SEQUENCE LISTING

<110> Liang, Yanbin Woodward, David F. <120> HUMAN COX-1 ALTERNATIVELY SPLICED VARIANTS AND METHODS OF USING SAME <130> 66872-028 (AR5746) <160> 38 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 2022 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (298)...(2022) <400> 1 atgageegga gtetettget eeggttettg etgtteetge teetgeteee geegeteeec 60 gtectgeteg eggacecagg ggegeecacg ecaggggeet etttgggagg aageegeagg 120 caccaaggga aatgagttcc ctttctccag cctctaaccg tctgggaacc catcctgatt 180 cccattgcca gtggagaagg tctcccctgg tgaagacttc gggagaacat gggagatgga 240 aatacattta ggagccggga tgcttcatct ggggtttaag agatccccat tgagcaa atg 300 Met agg aaa cog agg ctc atg aat coc tgt tgt tac tat cca tgc cag cac 348 Arg Lys Pro Arg Leu Met Asn Pro Cys Cys Tyr Tyr Pro Cys Gln His 10 5 15 cag ggc atc tgt gtc cgc ttc ggc ctt gac cgc tac cag tgt gac tgc 396 Gln Gly Ile Cys Val Arg Phe Gly Leu Asp Arg Tyr Gln Cys Asp Cys 20 25 acc ege acg gge tat tee gge eee aac tge ace ate eet gge etg tgg 444 Thr Arg Thr Gly Tyr Ser Gly Pro Asn Cys Thr Ile Pro Gly Leu Trp 35 40 acc tgg ctc cgg aat tca ctg cgg ccc agc ccc tct ttc acc cac ttc 492 Thr Trp Leu Arg Asn Ser Leu Arg Pro Ser Pro Ser Phe Thr His Phe 55 ctg ctc act cac ggg cgc tgg ttc tgg gag ttt gtc aat gcc acc ttc Leu Leu Thr His Gly Arg Trp Phe Trp Glu Phe Val Asn Ala Thr Phe 70

atc cga gag atg ctc atg cgc ctg gta ctc aca gtg cgc tcc aac ctt

Ile Arg Glu Met Leu Met Arg Leu Val Leu Thr Val Arg Ser Asn Leu ate eee agt eee eee ace tac aac tea gea cat gae tac ate age tgg 636 Ile Pro Ser Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile Ser Trp 100 105 gag tot tto too aac gtg ago tat tac act cgt att ctg ccc tot gtg 684 Glu Ser Phe Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro Ser Val 115 120 cct aaa gat tgc ccc aca ccc atg gga acc aaa ggg aag aag cag ttg 732 Pro Lys Asp Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys Gln Leu 130 135 cca gat gcc cag ctc ctg gcc cgc cgc ttc ctg ctc agg agg aag ttc 780 Pro Asp Ala Gln Leu Leu Ala Arg Arg Phe Leu Leu Arg Arg Lys Phe ata cct gac ccc caa ggc acc aac ctc atg ttt gcc ttc ttt gca caa 828 Ile Pro Asp Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe Ala Gln 165 170 cac ttc acc cac cag ttc ttc aaa act tct ggc aag atg ggt cct ggc 876 His Phe Thr His Gln Phe Phe Lys Thr Ser Gly Lys Met Gly Pro Gly 185 180 tte acc aag gcc ttg ggc cat ggg gta gac ctc ggc cac att tat gga Phe Thr Lys Ala Leu Gly His Gly Val Asp Leu Gly His Ile Tyr Gly 195 gac aat ctg gag cgt cag tat caa ctg cgg ctc ttt aag gat ggg aaa Asp Asn Leu Glu Arg Gln Tyr Gln Leu Arg Leu Phe Lys Asp Gly Lys 210 ctc aag tac cag gtg ctg gat gga gaa atg tac ccg ccc tcg gta gaa Leu Lys Tyr Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser Val Glu 230 235 gag gcg cet gtg ttg atg cae tae eec ega gge ate eeg eec eag age 1068 Glu Ala Pro Val Leu Met His Tyr Pro Arg Gly Ile Pro Pro Gln Ser 245 250 255 cag atg gct gtg ggc cag gag gtg ttt ggg ctg ctt cct ggg ctc atg 1116 Gln Met Ala Val Gly Gln Glu Val Phe Gly Leu Leu Pro Gly Leu Met 260 265 ctg tat gcc acg ctc tgg cta cgt gag cac aac cgt gtg tgt gac ctg 1164 Leu Tyr Ala Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys Asp Leu 275 280 ctg aag gct gag cac ccc acc tgg ggc gat gag cag ctt ttc cag acg 1212 Leu Lys Ala Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe Gln Thr 290 300 295

acc ege etc atc etc ata ggg gag acc atc aaq att qtc atc qaq qaq Thr Arg Leu Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Glu 310 315 tac gtg cag cag ctg agt ggc tat ttc ctg cag ctg aaa ttt gac cca 1308 Tyr Val Gln Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe Asp Pro 325 330 gag ctg ctg ttc ggt gtc cag ttc caa tac cgc aac cgc att gcc atg 1356 Glu Leu Leu Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile Ala Met gag ttc aac cat etc tac cac tqq cac ecc etc atq ect qac tec tte 1404 Glu Phe Asn His Leu Tyr His Trp His Pro Leu Met Pro Asp Ser Phe 360 365 aag gtg ggc tcc cag gag tac agc tac gag cag ttc ttg ttc aac acc 1452 Lys Val Gly Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe Asn Thr 370 375 tee atg ttg gtg gae tat ggg gtt gag gee etg gtg gat gee tte tet 1500 Ser Met Leu Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala Phe Ser 390 cgc cag att gct ggc cgg atc ggt ggg ggc agg aac atg gac cac cac 1548 Arg Gln Ile Ala Gly Arg Ile Gly Gly Gly Arg Asn Met Asp His His atc ctg cat gtg gct gtg gat gtc atc agg gag tct cgg gag atg cgg Ile Leu His Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu Met Arg 420 425 ctg cag ccc ttc aat gag tac cgc aag agg ttt ggc atg aaa ccc tac 1644 Leu Gln Pro Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys Pro Tyr 435 440 acc tcc ttc cag gag ctc gta gga gag aag gag atg gca gag ttg 1692 Thr Ser Phe Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala Glu Leu 450 465 gag gaa ttg tat gga gac att gat gcg ttg gag ttc tac cct gga ctg 1740 Glu Glu Leu Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly Leu ctt ctt gaa aag tgc cat cca aac tct atc ttt ggg gag agt atg ata 1788 Leu Leu Glu Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser Met Ile 485 490 gag att ggg gct ccc ttt tcc ctc aag ggt ctc cta ggg aat ccc atc 1836 Glu Ile Gly Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro Ile 500 505 tgt tct ccg gag tac tgg aag ccg agc aca ttt ggc ggc gag gtg ggc Cys Ser Pro Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly 515 520

ttt aac att gtc aag acg gcc aca ctg aag aag ctg gtc tgc ctc aac 1932
Phe Asn Ile Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys Leu Asn 530

acc aag acc tgt ccc tac gtt tcc ttc cgt gtg ccg gat gcc agt cag 1980
Thr Lys Thr Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala Ser Gln 550

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565

1932

2022

<210> 2 <211> 574 <212> PRT <213> Homo sapiens

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Leu Leu Lys Ala Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe Gln 295 300 Thr Thr Arg Leu Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu 310 315 Glu Tyr Val Gln Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe Asp 330 Pro Glu Leu Leu Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile Ala 345 Met Glu Phe Asn His Leu Tyr His Trp His Pro Leu Met Pro Asp Ser 365 360 Phe Lys Val Gly Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe Asn 375 Thr Ser Met Leu Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala Phe 390 395 Ser Arg Gln Ile Ala Gly Arg Ile Gly Gly Arg Asn Met Asp His 410 405 His Ile Leu His Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu Met 420 425 430 Arg Leu Gln Pro Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys Pro 440 Tyr Thr Ser Phe Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala Glu 455 Leu Glu Glu Leu Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly 470 475 Leu Leu Glu Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser Met 485 490 Ile Glu Ile Gly Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro 505 510 500 Ile Cys Ser Pro Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val 520 Gly Phe Asn Ile Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys Leu 535 540 Asn Thr Lys Thr Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala Ser 550 555 Gln Asp Asp Gly Pro Ala Val Glu Arg Pro Ser Thr Glu Leu 565 570 <210> 3 <211> 1818 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (298)...(1620) <400> 3 atgageegga gtetettget eeggttettg etgtteetge teetgeteee geegeteeee 60 gtcctgctcg cggacccagg ggcgcccacg ccaggggcct ctttgggagg aagccgcagg 120 caccaaggga aatgagttcc ctttctccag cctctaaccq tctgggaacc catcctgatt 180 cccattgcca gtggagaagg tctcccctgg tgaagacttc gggagaacat gggagatgga 240 aatacattta ggagccggga tgcttcatct ggggtttaag agatccccat tgagcaa atg 300

Met Leu Tyr Ala Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys Asp

280

275

Met 1

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	ctc Leu												444
	act Thr												492
	gta Val	-											540
	ctg Leu			_	-				_		-		588
 	gaa Glu 100	_	_										636
	ccc Pro	_		_		_							684
	ttt Phe												732
-	gag Glu		_		_	_	_	_	_	_			780
	ggc Gly												828
	acc Thr 180												876
	ttc Phe												924

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gag cga cca tcc aca gag ctc tga ggggcaggaa agcagcattc tggaggggag 1650 Glu Arg Pro Ser Thr Glu Leu * 435 440

agctttgtgc ttgtcattcc agagtgctga ggccagggct gatggtctta aatgctcatt 1710 ttctggtttg gcatggtgag tgttggggtt gacatttaga actttaagtc tcacccatta 1770 tctggaatat tgtgattctg tttattcttc cagaatgctg aactcctt 1818

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Leu Val Gly Glu Lys Glu Met Ala Ala Glu Leu Glu Glu Leu Tyr Gly 330 325 Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly Leu Leu Glu Lys Cys 345 340 His Pro Asn Ser Ile Phe Gly Glu Ser Met Ile Glu Ile Gly Ala Pro 360 Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro Ile Cys Ser Pro Glu Tyr 375 380 Trp Lys Pro Ser Thr Phe Gly Glu Val Gly Phe Asn Ile Val Lys 390 395 Thr Ala Thr Leu Lys Lys Leu Val Cys Leu Asn Thr Lys Thr Cys Pro 410 Tyr Val Ser Phe Arg Val Pro Asp Ala Ser Gln Asp Asp Gly Pro Ala 430 425 Val Glu Arg Pro Ser Thr Glu Leu 435 <210> 5 <211> 2109 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (298)...(1911) <400> 5 atgageegga gtetettget eeggttettg etgtteetge teetgeteee geegeteeee 60 gtectgeteg eggacecagg ggegeecacg ecaggggeet etttgggagg aageegeagg 120 caccaaggga aatgagttcc ctttctccag cctctaaccg tctgggaacc catcctgatt 180 cccattgcca gtggagaagg tctcccctgg tgaagacttc gggagaacat gggagatgga 240 aatacattta qqaqccqqqa tqcttcatct qqqqtttaaq aqatccccat tqaqcaa atg 300 Met agg aaa eeg agg ete atg aat eee tgt tgt tae tat eea tge eag eac 348 Arg Lys Pro Arg Leu Met Asn Pro Cys Cys Tyr Tyr Pro Cys Gln His 5 10 cag ggc atc tgt gtc cgc ttc ggc ctt gac cgc tac cag tgt gac tgc Gln Gly Ile Cys Val Arg Phe Gly Leu Asp Arg Tyr Gln Cys Asp Cys 20 25 ace ege acg gge tat tee gge eee aac tge ace ate eet gge etg tgg 444 Thr Arg Thr Gly Tyr Ser Gly Pro Asn Cys Thr Ile Pro Gly Leu Trp 35 40 acc tgg ctc cgg aat tca ctg cgg ccc agc ccc tct ttc acc cac ttc 492 Thr Trp Leu Arg Asn Ser Leu Arg Pro Ser Pro Ser Phe Thr His Phe 55 ctg ctc act cac ggg cgc tgg ttc tgg gag ttt gtc aat gcc acc ttc Leu Leu Thr His Gly Arg Trp Phe Trp Glu Phe Val Asn Ala Thr Phe 70 75

												gtg Val					588	
			_							_		gac Asp					636	
							_					att Ile 125					684	
,												gly ggg					732	
												ctc Leu					780	
												gcc Ala					828	
					_							aag Lys	_				876	
												ggc Gly 205					924	
												ttt Phe					972	
		_				Leu			Glu		Tyr	ccg Pro		Ser		Glu	1020	
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	Leu	Tyr 275	Ala	Thr	Leu	Trp	Leu 280	Arg	Glu	His	Asn	cgt Arg 285	Val	Cys	Asp	Leu	1164	
	_	_	-	_								cag Gln					1212	

										300					303	
						Gly 999										1260
		-	_	-		ggc										1308
	-	_			-	cag Gln										1356
						cac His 360										1404
						aac Asn										1452
	_	_				tct Ser			_		_	_				1500
		-	_			ggc Gly	_							_		1548
	_			_		atg Met	-	_		_		_	_			1596
_		_		_		ttc Phe 440				_			-	_	-	1644
						gl ^à aaa										1692
			-			cta Leu					_		_			1740
	-	_	_			ggc Gly		-						_	-	1788
-	-		_	-		ctg Leu						-		-		1836
tac	gtt	tcc	ttc	cgt	gtg	ccg	gat	gcc	agt	cag	gat	gat	aa a	cct	gct	1884

Tyr Val Ser Phe Arg Val Pro Asp Ala Ser Gln Asp Asp Gly Pro Ala 515 520 525

gtg gag cga cca tcc aca gag ctc tga ggggcaggaa agcagcattc 1931 Val Glu Arg Pro Ser Thr Glu Leu * 530 535

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<210> 6 <211> 537 <212> PRT <213> Homo sapiens

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Thr Thr Arg Leu Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu 305 310 315 Glu Tyr Val Gln Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe Asp 325 330 Pro Glu Leu Leu Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile Ala 345 Met Glu Phe Asn His Leu Tyr His Trp His Pro Leu Met Pro Asp Ser 360 Phe Lys Ile Gly Gly Arg Asn Met Asp His His Ile Leu His Val 375 380 Ala Val Asp Val Ile Arg Glu Ser Arg Glu Met Arg Leu Gln Pro Phe 390 395 Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys Pro Tyr Thr Ser Phe Gln 405 410 Glu Leu Val Gly Glu Lys Glu Met Ala Ala Glu Leu Glu Glu Leu Tyr 420 425 Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly Leu Leu Leu Glu Lys 440 Cys His Pro Asn Ser Ile Phe Gly Glu Ser Met Ile Glu Ile Gly Ala 455 460 Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro Ile Cys Ser Pro Glu 470 475 Tyr Trp Lys Pro Ser Thr Phe Gly Glu Val Gly Phe Asn Ile Val 490 485 Lys Thr Ala Thr Leu Lys Lys Leu Val Cys Leu Asn Thr Lys Thr Cys 505 510 Pro Tyr Val Ser Phe Arg Val Pro Asp Ala Ser Gln Asp Asp Gly Pro 520 Ala Val Glu Arg Pro Ser Thr Glu Leu 530 535 <210> 7 <211> 2280 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (298)...(2082) <400> 7 atgageegga gtetettget eeggttettg etgtteetge teetgeteee geegeteeee 60 qtcctqctcq cqqacccaqq qqcqccacq ccaqqqqcct ctttqqqaqq aaqccqcaqq 120 caccaaggga aatgagttcc ctttctccag cctctaaccg tctgggaacc catcctgatt 180 cccattgcca gtggagaagg tctcccctgg tgaagacttc gggagaacat gggagatgga 240 aatacattta ggagccggga tgcttcatct ggggtttaag agatccccat tgagcaa atg 300 Met agg aaa ccg agg ctc agt agg tgc cat gat tcc cca agc tca caa aat Arg Lys Pro Arg Leu Ser Arg Cys His Asp Ser Pro Ser Ser Gln Asn aca tgg tgg gcc cag gat ctg aac tca gtg aat ccc tgt tgt tac tat

Thr Trp Trp Ala Gln Asp Leu Asn Ser Val Asn Pro Cys Cys Tyr Tyr cca tgc cag cac cag ggc atc tgt gtc cgc ttc ggc ctt gac cgc tac Pro Cys Gln His Gln Gly Ile Cys Val Arg Phe Gly Leu Asp Arg Tyr 492 caq tqt qac tqc acc cqc acq qqc tat tcc qqc ccc aac tqc acc atc Gln Cys Asp Cys Thr Arg Thr Gly Tyr Ser Gly Pro Asn Cys Thr Ile 55 cet gge etg tgg ace tgg ete egg aat tea etg egg eee age eee tet 540 Pro Gly Leu Trp Thr Trp Leu Arg Asn Ser Leu Arg Pro Ser Pro Ser 70 75 tte ace cae tte etg ete act cae ggg ege tgg tte tgg gag ttt gte 588 Phe Thr His Phe Leu Leu Thr His Gly Arg Trp Phe Trp Glu Phe Val aat qcc acc ttc atc cga gag atg ctc atg cgc ctg gta ctc aca gtg Asn Ala Thr Phe Ile Arg Glu Met Leu Met Arg Leu Val Leu Thr Val 105 cgc tcc aac ctt atc ccc agt ccc ccc acc tac aac tca gca cat gac 684 Arg Ser Asn Leu Ile Pro Ser Pro Pro Thr Tyr Asn Ser Ala His Asp 115 120 tac atc agc tgg gag tct ttc tcc aac gtg agc tat tac act cgt att 732 Tyr Ile Ser Trp Glu Ser Phe Ser Asn Val Ser Tyr Tyr Thr Arg Ile 130 135 140 ctg ccc tct gtg cct aaa gat tgc ccc aca ccc atg gga acc aaa ggg 780 Leu Pro Ser Val Pro Lys Asp Cys Pro Thr Pro Met Gly Thr Lys Gly 150 aaq aaq caq ttq cca qat qcc caq ctc ctq qcc cgc cgc ttc ctg ctc Lys Lys Gln Leu Pro Asp Ala Gln Leu Leu Ala Arg Arg Phe Leu Leu 165 170 agg agg aag ttc ata cct gac ccc caa ggc acc aac ctc atg ttt gcc 876 Arg Arg Lys Phe Ile Pro Asp Pro Gln Gly Thr Asn Leu Met Phe Ala tte ttt gea caa cae tte ace cae cag tte tte aaa act tet gge aag 924 Phe Phe Ala Gln His Phe Thr His Gln Phe Phe Lys Thr Ser Gly Lys 195 200 atg ggt cct ggc ttc acc aag gcc ttg ggc cat ggg gta gac ctc ggc 972 Met Gly Pro Gly Phe Thr Lys Ala Leu Gly His Gly Val Asp Leu Gly 220 210 215 225 cac att tat gga gac aat ctg gag cgt cag tat caa ctg cgg ctc ttt 1020 His Ile Tyr Gly Asp Asn Leu Glu Arg Gln Tyr Gln Leu Arg Leu Phe 230

aag gat gg Lys Asp Gl				Leu Asp			
ccc tcg gt Pro Ser Va 20				_			
ccg ccc ca Pro Pro Gl 275			Val Gly				
cct ggg ct Pro Gly Le 290		-			Arg Glu		
gtg tgt ga Val Cys As		Lys Ala					_
ctt ttc ca	-	-		lle Gly		_	
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aaa ttt ga Lys Phe A 355			Phe Gly				
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95

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